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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=9; day=23; hr=13; min=47; sec=2; ms=955;]

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Reviewer Comments:

<210> 3

<211> 1647

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<223> GroEL-Asp490Cys DNA sequence

<220>

<221> mutation

<222> (1468)..(1470)

<223> GAC to TCG

<400> 3

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The above <223> response describing the base mutation at location 1468-1470 is incorrect: the mutation is "tgc" not "tcg".

Application No: 10583179 Version No: 1.0

Input Set:

Output Set:

Started: 2008-08-25 16:14:49.870

Finished: 2008-08-25 16:14:50.245

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 375 ms

Total Warnings: 0

Total Errors: 0

No. of SeqIDs Defined: 8

Actual SeqID Count: 8

SEQUENCE LISTING

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<120> Protein Separation Device

<130> 51571-4

<140> 10583179

<141> 2008-08-25

<150> US 60/530,608

<151> 2003-12-19

<160> 8

<170> PatentIn version 3.3

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<211> 1647

<212> DNA

<213> Escherichia coli

<220>

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<212> PRT

<213> Escherichia coli

<220>

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<223> GroEL wildtype amino acid sequence

<400> 2

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35 40 45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp

50 55 60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys

65 70 75 80

Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala

85 90 95

Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn

100 105 110

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val

115 120 125

Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile

130 135 140

Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys

145 150 155 160

Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr

165 170 175

Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp Val Val Glu Gly

180 185 190

Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro

195 200 205

Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp

210 215 220

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Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met						
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	290			295		300
Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp Leu Gly Gln Ala						
	305			310		315
Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile Ile Asp Gly Val						
	325			330		335
Gly Glu Glu Ala Ala Ile Gln Gly Arg Val Ala Gln Ile Arg Gln Gln						
	340			345		350
Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg						
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Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala						
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Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu						
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His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly						
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Val Ala Leu Ile Arg Val Ala Ser Lys Leu Ala Asp Leu Arg Gly Gln						
	420			425		430
Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu						
	435			440		445
Ala Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val						
	450			455		460
Val Ala Asn Thr Val Lys Gly Gly Asp Gly Asn Tyr Gly Tyr Asn Ala						
	465			470		475
Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly Ile Leu Asp Pro						
	485			490		495
Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly						
	500			505		510
Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Asn Asp						
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530 535 540

Gly Gly Met Met
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<210> 3
<211> 1647
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<223> GroEL-Asp490Cys DNA sequence

<220>
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<223> GAC to TCG

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<211> 548
<212> PRT
<213> Escherichia coli

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Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
35          40          45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
50          55          60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
65          70          75          80

Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
85          90          95

Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
100         105         110

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val
115         120         125

Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile
130         135         140

Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys
145         150         155         160

Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr
165         170         175

Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp Val Val Glu Gly
180         185         190

Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro
195         200         205

Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp
210         215         220

Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val
225         230         235         240

Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly
245         250         255

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Ile	Gly	Met	Glu	Leu	Glu	Lys	Ala	Thr	Leu	Glu	Asp	Leu	Gly	Gln	Ala	305	310	315
Lys	Arg	Val	Val	Ile	Asn	Lys	Asp	Thr	Thr	Thr	Ile	Ile	Asp	Gly	Val	325	330	335
Gly	Glu	Glu	Ala	Ala	Ile	Gln	Gly	Arg	Val	Ala	Gln	Ile	Arg	Gln	Gln	340	345	350
Ile	Glu	Glu	Ala	Thr	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	355	360	365
Val	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	370	375	380
Thr	Glu	Val	Glu	Met	Lys	Glu	Lys	Lys	Ala	Arg	Val	Glu	Asp	Ala	Leu	385	390	395
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Ala	Pro	Leu	Arg	Gln	Ile	Val	Leu	Asn	Cys	Gly	Glu	Glu	Pro	Ser	Val	450	455	460
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Ala	Thr	Glu	Glu	Tyr	Gly	Asn	Met	Ile	Cys	Met	Gly	Ile	Leu	Asp	Pro	485	490	495
Thr	Lys	Val	Thr	Arg	Ser	Ala	Leu	Gln	Tyr	Ala	Ala	Ser	Val	Ala	Gly	500	505	510
Leu	Met	Ile	Thr	Thr	Glu	Cys	Met	Val	Thr	Asp	Leu	Pro	Lys	Asn	Asp	515	520	525
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 <222> (598)..(606)
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<220>
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20 25 30

Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
35 40 45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
50 55 60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
65 70 75 80

Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala T